

**Figure 1**

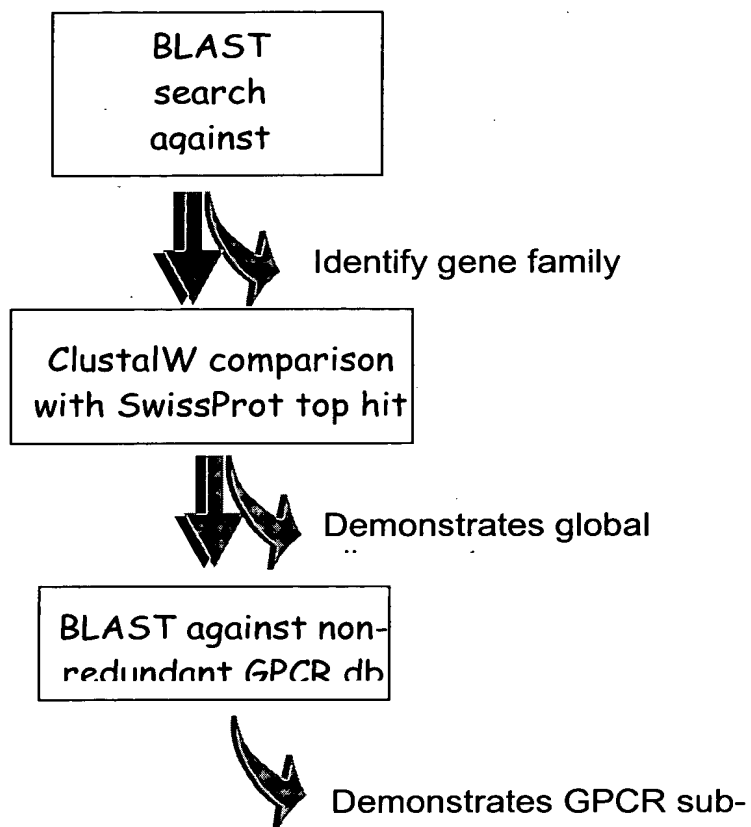


Figure 2

ClustalW Alignment of PFI-017 with Cysteinyl Leukotriene Receptor

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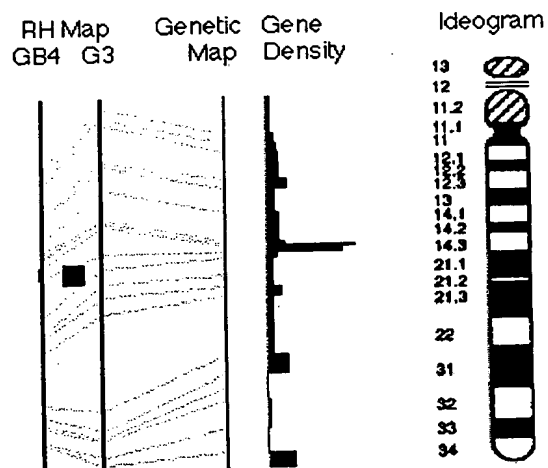
1                                                                 70
PFI-017 (1) M P N G T F S N N - N S R N C T L E N F K R E F E P I V Y L I F F W G V L G N G L S T Y V F L O P Y K K S T S V N V E M N L A I S D L
CysLT1 (1) M D E T G N L I V S S A I C H D T I D D E R N Q V M S T E Y S M I S V V G F F G N G F V I Y V L I K T Y H K K S A F Q V Y M I N L A V A D L
Consensus (1) M D G S S T I D F K F L Y I I G G N G I Y V I Y K S A N V F M I N L A I A D L
71                                                                 140
PFI-017 (70) L F I S T L P F R A D Y Y I R G S N W E G D L A C R T M S Y S L Y V N M Y S S I F E T V E S V V R F E A M V H P F R L L H V T S I R S A
CysLT1 (71) L C V C T L P L R V V Y V H K G I W E G D F L C R T S E Y A L Y V N L Y C S I E F M T A M S F F R C L A T V F R V Q N I N V I H K K A
Consensus (71) L I T L P R Y Y L W I F G D C R I S Y A L Y V N L Y S I F F L T L S R I A I V P I L S K A
141                                                                 210
PFI-017 (140) W I P G I I W I L E M A S S I M L D S G S E Q N - G S V T S C L E L N L Y K I A K - - E Q T M N Y T A L V V G C L P P F F T E S I C Y L
CysLT1 (141) R F V C V G E W I F V L L I S S P F L M A K P Q K D E K N N T K C F E P P Q D N Q T K N H L V E H Y S L F V G F L P P F V I I I C Y T
Consensus (141) L C I W I I I S S L A T C E K L L Y I A L V G I I P F I I C Y
211                                                                 280
PFI-017 (207) E I I R V L L K V E P E S G L R V S H R K A I T T I I I T L I I F F E C F P P Y H T L R T V H L T T W K - - V G L C K - - D R I H K A L V
CysLT1 (211) M I I L T L L K K S M K K N - - L S S H K K A I G M I M V T A A F L S F M P Y H I Q R T E H L H F L H N E T K P C D S V L R M Q K S V V
Consensus (211) L I I L L K M S H K K A I I I F L F L P Y H R T I H L C R L K A L V
281                                                                 340
PFI-017 (273) I T L A L A A N A C F N P L L Y F A G E N F K D R L K S A L R K G H P Q A K T K C V F P V S V W L R K E T R V - -
CysLT1 (279) I T L S L A A S N C C F D P L L Y E F S G G N F K R L S - T F R K H S L S S V T Y V P R K K A S I P E K G E E I C K V
Consensus (281) I T L A L A A N C F P L L Y F F A G N F K R L R K S L K E

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Figure 3

5



10

103070 1623660

**Figure 4**

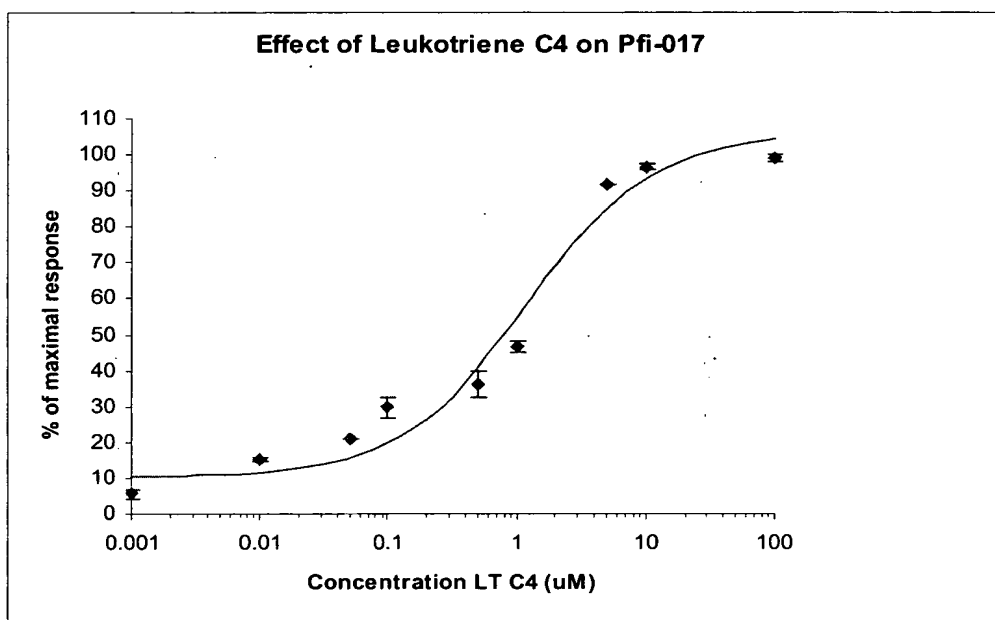
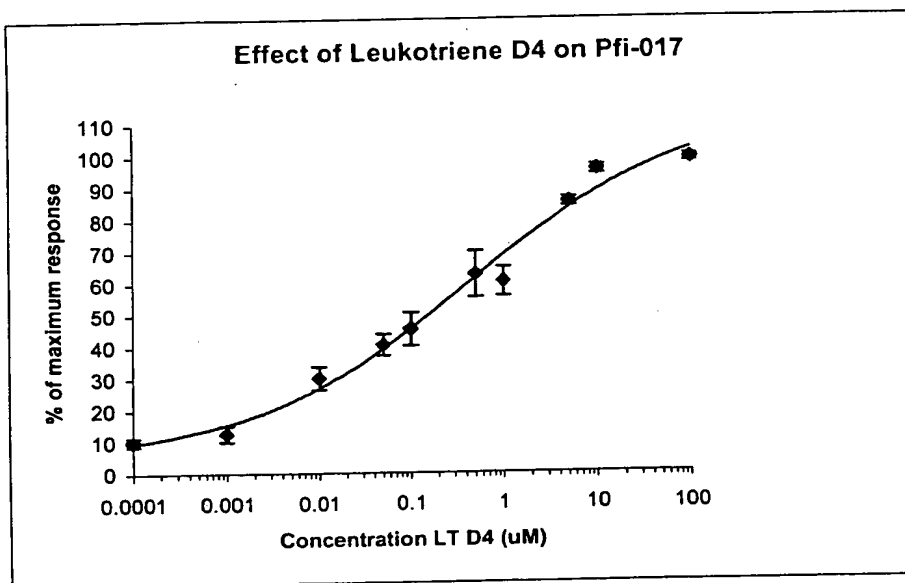


Figure 5



5

10

103040 " 1523360

**Figure 6A**

(SEQ ID NO: 1)

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attttaaggacagactaaagtctgcactcagaaaaggccatccacagaaggcaaaagacaaagtgtgtttccctgttagtgtgtgg  
ttgagaaaggaaacaagagtataa

**Figure 6B**

(SEQ ID NO: 2)

Met Glu Pro Asn Gly Thr Phe Ser Asn Asn Asn Ser Arg Asn Cys Thr  
Ile Glu Asn Phe Lys Arg Glu Phe Phe Pro Ile Val Tyr Leu Ile Ile  
Phe Phe Trp Gly Val Leu Gly Asn Gly Leu Ser Ile Tyr Val Phe Leu  
Gln Pro Tyr Lys Lys Ser Thr Ser Val Asn Val Phe Met Leu Asn Leu  
Ala Ile Ser Asp Leu Leu Phe Ile Ser Thr Leu Pro Phe Arg Ala Asp  
Tyr Tyr Leu Arg Gly Ser Asn Trp Ile Phe Gly Asp Leu Ala Cys Arg  
Ile Met Ser Tyr Ser Leu Tyr Val Asn Met Tyr Ser Ser Ile Tyr Phe  
Leu Thr Val Leu Ser Val Val Arg Phe Leu Ala Met Val His Pro Phe  
Arg Leu Leu His Val Thr Ser Ile Arg Ser Ala Trp Ile Leu Cys Gly  
Ile Ile Trp Ile Leu Ile Met Ala Ser Ser Ile Met Leu Leu Asp Ser  
Gly Ser Glu Gln Asn Gly Ser Val Thr Ser Cys Leu Glu Leu Asn Leu  
Tyr Lys Ile Ala Lys Leu Gln Thr Met Asn Tyr Ile Ala Leu Val Val  
Gly Cys Leu Leu Pro Phe Phe Thr Leu Ser Ile Cys Tyr Leu Leu Ile  
Ile Arg Val Leu Leu Lys Val Glu Val Pro Glu Ser Gly Leu Arg Val  
Ser His Arg Lys Ala Leu Thr Thr Ile Ile Ile Thr Leu Ile Ile Phe  
Phe Leu Cys Phe Leu Pro Tyr His Thr Leu Arg Thr Val His Leu Thr  
Thr Trp Lys Val Gly Leu Cys Lys Asp Arg Leu His Lys Ala Leu Val  
Ile Thr Leu Ala Leu Ala Ala Ala Asn Ala Cys Phe Asn Pro Leu Leu  
Tyr Tyr Phe Ala Gly Glu Asn Phe Lys Asp Arg Leu Lys Ser Ala Leu  
Arg Lys Gly His Pro Gln Lys Ala Lys Thr Lys Cys Val Phe Pro Val  
Ser Val Trp Leu Arg Lys Glu Thr Arg Val

**Figure 7A**

(SEQ ID NO: 5)

atggagagaaaatttatgtccttgcaaccatccatctccgtatcagaaatggaaccaaattggcaccttcagcaataacaacagca  
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gcagccaatgctgcttcaatcctctgctctattacttctgtggggagaatttaaggacagactaaagtctgcactcagaaaaggc  
catccacagaaggcaagacaaagtgtgtttccctgttagtgtgtgttgagaaaggaaacaagagtataa

**Figure 7B**

(SEQ ID NO: 6)

Met Glu Arg Lys Phe Met Ser Leu Gln Pro Ser Ile Ser Val Ser Glu  
Met Glu Pro Asn Gly Thr Phe Ser Asn Asn Asn Ser Arg Asn Cys Thr  
Ile Glu Asn Phe Lys Arg Glu Phe Phe Pro Ile Val Tyr Leu Ile Ile  
Phe Phe Trp Gly Val Leu Gly Asn Gly Leu Ser Ile Tyr Val Phe Leu  
Gln Pro Tyr Lys Lys Ser Thr Ser Val Asn Val Phe Met Leu Asn Leu  
Ala Ile Ser Asp Leu Leu Phe Ile Ser Thr Leu Pro Phe Arg Ala Asp  
Tyr Tyr Leu Arg Gly Ser Asn Trp Ile Phe Gly Asp Leu Ala Cys Arg  
Ile Met Ser Tyr Ser Leu Tyr Val Asn Met Tyr Ser Ser Ile Tyr Phe  
Leu Thr Val Leu Ser Val Val Arg Phe Leu Ala Met Val His Pro Phe  
Arg Leu Leu His Val Thr Ser Ile Arg Ser Ala Trp Ile Leu Cys Gly  
Ile Ile Trp Ile Leu Ile Met Ala Ser Ser Ile Met Leu Leu Asp Ser  
Gly Ser Glu Gln Asn Gly Ser Val Thr Ser Cys Leu Glu Leu Asn Leu  
Tyr Lys Ile Ala Lys Leu Gln Thr Met Asn Tyr Ile Ala Leu Val Val  
Gly Cys Leu Leu Pro Phe Phe Thr Leu Ser Ile Cys Tyr Leu Leu Ile  
Ile Arg Val Leu Leu Lys Val Glu Val Pro Glu Ser Gly Leu Arg Val  
Ser His Arg Lys Ala Leu Thr Thr Ile Ile Ile Thr Leu Ile Ile Phe  
Phe Leu Cys Phe Leu Pro Tyr His Thr Leu Arg Thr Val His Leu Thr  
Thr Trp Lys Val Gly Leu Cys Lys Asp Arg Leu His Lys Ala Leu Val  
Ile Thr Leu Ala Leu Ala Ala Ala Asn Ala Cys Phe Asn Pro Leu Leu  
Tyr Tyr Phe Ala Gly Glu Asn Phe Lys Asp Arg Leu Lys Ser Ala Leu  
Arg Lys Gly His Pro Gln Lys Ala Lys Thr Lys Cys Val Phe Pro Val  
Ser Val Trp Leu Arg Lys Glu Thr Arg Val